

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 09/920,705A
Source: IFW/6
Date Processed by STIC: 5/18/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 05/18/2006

PATENT APPLICATION: US/09/920,705A

TIME: 11:03:06

Input Set : A:\960296.97214 - Sequence Listing.txt

Output Set: N:\CRF4\05182006\I920705A.raw

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3 <110> APPLICANT: Amasino, Richard M.
4     Schomburg, Fritz M.
5     Michaels, Scott D.
6     Patton, David
8 <120> TITLE OF INVENTION: FLORAL INDUCTION GENE
10 <130> FILE REFERENCE: 960296.97214
12 <140> CURRENT APPLICATION NUMBER: 09/920,705A
13 <141> CURRENT FILING DATE: 2001-08-02
15 <150> PRIOR APPLICATION NUMBER: US 60/222,550
16 <151> PRIOR FILING DATE: 2000-08-03
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4593
24 <212> TYPE: DNA
25 <213> ORGANISM: Arabidopsis thaliana
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32 tacggcgata ttgatagaat cacggtgtat tcttcacgag gctttgcgtt tatatactac      180
34 agacatgtgg aggaagcagt cgcagccaaa gaggctcttc aaggagcaaa tttgaatgga      240
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40 tcacaaaact ttgatgatgc ttgttttagtc caaaaatttc ttgttgaatc tgtttttttt      420
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46 cgcgcaaagc caaaccacag agaagctctg caaaatttga tgttaaagca tatataactc      600
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56 taagaaattt tggagtttaa aagttcagtt tcctgcaaaa atcaaaccgc gtggagaaat      900
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60 ccgtatcgtc ctaactccta gtatcgctgg cacatatcca tatcagtggtg agggagtttt     1020
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92 aaacgctcca gtaaacattt tgtttagttt cataatttgc gtcaaactga tagggctgag 1980
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128 gtggaactcc cgtctgttgt gctcgttgtg tacctatggg aaaggggatt gaaactaaac 3060
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138 gtcaatttgt cagcaagaac tgatttgaat atgctcgcta aacattacgc cgttgccatt 3360
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172 ggcgtaacaa caaatcaggc acagaactta aacccttccc aatttcaagc tgccatgcaa 4380
174 ccaccagcag ataaggcaaa tttagagcca caaaaccaag cactacgatt gcagcctatg 4440
176 atctctgggg atggtcaggg tacaacagat ggggaggtcg ataagaatca gagataccag 4500

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178 tcaacactac aatttgcagc aaaccttctt ctccagatac agcagaaaca gcagcaacag      4560
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193 <220> FEATURE:
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208 1          5          10          15
210 tca aac aat ctt tgg gtc ggt agc cta acg ccg gag acg aca gag tca      96
211 Ser Asn Asn Leu Trp Val Gly Ser Leu Thr Pro Glu Thr Thr Glu Ser
212          20          25          30
214 gat ctg acc gag ttg ttt gga aga tac ggc gat att gat aga atc acg      144
215 Asp Leu Thr Glu Leu Phe Gly Arg Tyr Gly Asp Ile Asp Arg Ile Thr
216          35          40          45
218 gtg tat tct tca cga ggc ttt gcg ttt ata tac tac aga cat gtg gag      192
219 Val Tyr Ser Ser Arg Gly Phe Ala Phe Ile Tyr Tyr Arg His Val Glu
220          50          55          60
222 gaa gca gtc gca gcc aaa gag gct ctt caa gga gca aat ttg aat gga      240
223 Glu Ala Val Ala Ala Lys Glu Ala Leu Gln Gly Ala Asn Leu Asn Gly
224 65          70          75          80
226 agt caa att aag atc gaa tac gca cga ccg gca aaa cct tgt aag agt      288
227 Ser Gln Ile Lys Ile Glu Tyr Ala Arg Pro Ala Lys Pro Cys Lys Ser
228          85          90          95
230 cta tgg gtg ggt gga atc ggc cct aat gtc tcc aag gat gac ctg gag      336
231 Leu Trp Val Gly Gly Ile Gly Pro Asn Val Ser Lys Asp Asp Leu Glu
232          100          105          110
234 gaa gag ttc agc aag ttt ggg aaa atc gag gat ttt agg ttt ctc aga      384
235 Glu Glu Phe Ser Lys Phe Gly Lys Ile Glu Asp Phe Arg Phe Leu Arg
236          115          120          125
238 gaa cgc aag aca gct ttc att gat tat tat gag atg gat gat gct tta      432
239 Glu Arg Lys Thr Ala Phe Ile Asp Tyr Tyr Glu Met Asp Asp Ala Leu
240          130          135          140
242 cag gct aag agc atg aat gga aag cct atg ggt agc ttt ttg cgt      480
243 Gln Ala Lys Ser Met Asn Gly Lys Pro Met Gly Ser Phe Leu Arg
244 145          150          155          160

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247	Val	Asp	Phe	Leu	Arg	Ser	Gln	Ala	Pro	Lys	Lys	Glu	Gln	Trp	Ala	Gly	
248				165						170				175			
250	tct	tac	gat	aac	aga	aat	ggc	aat	atg	aat	cat	aaa	ccg	cag	tat	cct	576
251	Ser	Tyr	Asp	Asn	Arg	Asn	Gly	Asn	Met	Asn	His	Lys	Pro	Gln	Tyr	Pro	
252				180					185					190			
254	cac	tca	tat	gaa	gac	ttt	aaa	gga	gat	gtc	cag	cca	agt	aag	gtt	ctg	624
255	His	Ser	Tyr	Glu	Asp	Phe	Lys	Gly	Asp	Val	Gln	Pro	Ser	Lys	Val	Leu	
256				195					200					205			
258	tgg	att	ggg	ttc	cct	cct	act	gct	aca	caa	tgc	aat	gat	gag	caa	att	672
259	Trp	Ile	Gly	Phe	Pro	Pro	Thr	Ala	Thr	Gln	Cys	Asn	Asp	Glu	Gln	Ile	
260		210						215						220			
262	ctg	cac	aat	gcg	atg	ata	ctc	ttt	ggg	gag	atc	gag	agg	gta	aaa	agt	720
263	Leu	His	Asn	Ala	Met	Ile	Leu	Phe	Gly	Glu	Ile	Glu	Arg	Val	Lys	Ser	
264	225					230				235				240			
266	tac	cca	tca	agg	aat	ttt	gca	ctt	gtg	gag	ttt	agg	agc	gcg	gag	gaa	768
267	Tyr	Pro	Ser	Arg	Asn	Phe	Ala	Leu	Val	Glu	Phe	Arg	Ser	Ala	Glu	Glu	
268					245					250				255			
270	gct	cgc	caa	tgc	aag	gaa	ggc	cta	cag	ggg	agg	tta	ttc	aat	aat	cct	816
271	Ala	Arg	Gln	Cys	Lys	Glu	Gly	Leu	Gln	Gly	Arg	Leu	Phe	Asn	Asn	Pro	
272				260					265					270			
274	aga	atc	aaa	att	atg	tac	tca	aac	gat	gag	ttg	cct	cct	gag	caa	gac	864
275	Arg	Ile	Lys	Ile	Met	Tyr	Ser	Asn	Asp	Glu	Leu	Pro	Pro	Glu	Gln	Asp	
276			275					280						285			
278	gat	act	agt	ttt	tac	tct	ggg	atg	aaa	cgg	tca	agg	aca	gat	atg	ttc	912
279	Asp	Thr	Ser	Phe	Tyr	Ser	Gly	Met	Lys	Arg	Ser	Arg	Thr	Asp	Met	Phe	
280		290					295					300					
282	aat	aat	gat	cct	tca	tgt	gta	tct	tct	cct	cat	tct	act	gga	att	cct	960
283	Asn	Asn	Asp	Pro	Ser	Cys	Val	Ser	Ser	Pro	His	Ser	Thr	Gly	Ile	Pro	
284	305				310					315				320			
286	ggg	tct	atg	agg	ccc	ctc	aga	ggg	acg	aat	gag	cgt	tca	tat	aat	ggg	1008
287	Gly	Ser	Met	Arg	Pro	Leu	Arg	Gly	Thr	Asn	Glu	Arg	Ser	Tyr	Asn	Gly	
288				325					330					335			
290	gca	gaa	tac	aat	gac	gtt	gtt	ggg	aag	gag	cca	aac	tgg	agg	agg	cca	1056
291	Ala	Glu	Tyr	Asn	Asp	Val	Val	Gly	Lys	Glu	Pro	Asn	Trp	Arg	Arg	Pro	
292				340					345					350			
294	tct	gca	aat	gga	act	gga	ata	ctc	cca	tct	cca	aca	gga	cct	gga	atc	1104
295	Ser	Ala	Asn	Gly	Thr	Gly	Ile	Leu	Pro	Ser	Pro	Thr	Gly	Pro	Gly	Ile	
296			355					360						365			
298	ctc	cca	tct	cct	gca	caa	ggg	acg	agg	cgc	cct	atg	agg	tca	aac	ccc	1152
299	Leu	Pro	Ser	Pro	Ala	Gln	Gly	Thr	Arg	Arg	Pro	Met	Arg	Ser	Asn	Pro	
300		370					375					380					
302	gat	tct	tgg	gaa	gga	tat	gat	cct	gct	cag	ttg	gtc	aga	gaa	agt	aaa	1200
303	Asp	Ser	Trp	Glu	Gly	Tyr	Asp	Pro	Ala	Gln	Leu	Val	Arg	Glu	Ser	Lys	
304	385				390					395				400			
306	cga	acc	aga	aga	gat	gga	tca	gtg	gac	ggg	ttt	act	cca	atg	ggg	gtc	1248
307	Arg	Thr	Arg	Arg	Asp	Gly	Ser	Val	Asp	Gly	Phe	Thr	Pro	Met	Gly	Val	
308				405					410					415			
310	gat	gag	agg	tca	ttt	ggg	cga	ggg	tca	gtt	gct	gct	aga	cct	atc	cgt	1296

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315 Gly Pro Pro Asp Ser Asp His Ile Trp Arg Gly Met Ile Ala Lys Gly
316          435          440          445
318 gga act ccc gtc tgt tgt gct cgt tgt gta cct atg gga aag ggg att      1392
319 Gly Thr Pro Val Cys Cys Ala Arg Cys Val Pro Met Gly Lys Gly Ile
320          450          455          460
322 gaa act aaa ctg cct gag gtc gtc aat tgt tca gca aga act gat ttg      1440
323 Glu Thr Lys Leu Pro Glu Val Val Asn Cys Ser Ala Arg Thr Asp Leu
324 465          470          475          480
326 aat atg ctc gct aaa cat tac gcc gtt gcc att gga tgt gag atc gtt      1488
327 Asn Met Leu Ala Lys His Tyr Ala Val Ala Ile Gly Cys Glu Ile Val
328          485          490          495
330 ttt ttc gta cca gac agg gaa gaa gat ttt gcg tct tac act gaa ttt      1536
331 Phe Phe Val Pro Asp Arg Glu Glu Asp Phe Ala Ser Tyr Thr Glu Phe
332          500          505          510
334 ctc cgg tac ctt agc tca aaa gat cgg gcg ggt gtt gcc aaa tta gat      1584
335 Leu Arg Tyr Leu Ser Ser Lys Asp Arg Ala Gly Val Ala Lys Leu Asp
336          515          520          525
338 gat ggt aca act tta ttc ttg gtg cct cca tca gat ttc tta act gat      1632
339 Asp Gly Thr Thr Leu Phe Leu Val Pro Pro Ser Asp Phe Leu Thr Asp
340          530          535          540
342 gta ctc caa gtg acc cgt caa gaa cgg cta tat ggt gtt gtt ctc aag      1680
343 Val Leu Gln Val Thr Arg Gln Glu Arg Leu Tyr Gly Val Val Leu Lys
344 545          550          555          560
346 tta ccc ccg cca gcc gtt cct gtt aca gca tca tac aga caa gaa tct      1728
347 Leu Pro Pro Pro Ala Val Pro Val Thr Ala Ser Tyr Arg Gln Glu Ser
348          565          570          575
350 cag tcc aat cct ctg cat tat atg gat caa gcc cgg gat tca cct gcc      1776
351 Gln Ser Asn Pro Leu His Tyr Met Asp Gln Ala Arg Asp Ser Pro Ala
352          580          585          590
354 aat gct agt cac agt tta tat cct cct agg gaa aat tac att agg ggt      1824
355 Asn Ala Ser His Ser Leu Tyr Pro Pro Arg Glu Asn Tyr Ile Arg Gly
356          595          600          605
358 gca cca gaa cat ttg aca gct gct tca aaa cca tct gtt agc gag cct      1872
359 Ala Pro Glu His Leu Thr Ala Ala Ser Lys Pro Ser Val Ser Glu Pro
360          610          615          620
362 ctc aga ata cct aat aat gca gcg cct caa gct ggg gtt agt tta act      1920
363 Leu Arg Ile Pro Asn Asn Ala Ala Pro Gln Ala Gly Val Ser Leu Thr
364 625          630          635          640
366 ccg gag ctt tta gcc act ctg gca tct att ctc cct gca act tct caa      1968
367 Pro Glu Leu Leu Ala Thr Leu Ala Ser Ile Leu Pro Ala Thr Ser Gln
368          645          650          655
370 cct gct gcc cct gag agt cac caa cct atg tca gga cct tca aca gtt      2016
371 Pro Ala Ala Pro Glu Ser His Gln Pro Met Ser Gly Pro Ser Thr Val
372          660          665          670
374 gtt tcc aca gca cat cag tcc aat gga ctg tac aat gga gaa gca ccg      2064
375 Val Ser Thr Ala His Gln Ser Asn Gly Leu Tyr Asn Gly Glu Ala Pro

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10

VERIFICATION SUMMARY

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